

SEQUENCE LISTING

<110> Afar, Daniel E. H.
 Hubert, Rene S.
 Leong, Kahan
 Raitano, Arthur B.
 Saffran, Douglas C.
 Mitchell, Stephen C.
 Jakobovits, Aya
 Faris, Mary
 Vivanco, Igo

<120> NOVEL TUMOR ANTIGEN USEFUL IN DIAGNOSIS
 AND THERAPY OF PROSTATE AND COLON CANCER

<130> 511582000820

<140> 09/615,285

<141> 2000-07-12

<150> 09/323,597

<151> 1999-06-01

<150> 60/087,598

<151> 1998-06-01

<150> 60/091,474

<151> 1998-06-29

<150> 60/129,521

<151> 1999-04-14

<160> 43

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1738

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (112)...(1588)

<400> 1

ggcggaggcg gagggcgagg gcgaggggccc gggagcgccc cctggagcgc ggcaggtcat 60
 attgaacatt ccagatacct atcattactc gatgctgttg ataacagcaa g atg gct 117
 Met Ala
 1

ttg aac tca ggg tca cca cca gct att gga cct tac tat gaa aac cat 165
 Leu Asn Ser Gly Ser Pro Pro Ala Ile Gly Pro Tyr Tyr Glu Asn His
 5 10 15

gga tac caa ccg gaa aac ccc tat ccc gca cag ccc act gtg gtc ccc 213
 Gly Tyr Gln Pro Glu Asn Pro Tyr Pro Ala Gln Pro Thr Val Val Pro
 20 25 30

act gtc tac gag gtg cat ccg gct cag tac tac ccg tcc ccc gtg ccc 261
 Thr Val Tyr Glu Val His Pro Ala Gln Tyr Tyr Pro Ser Pro Val Pro
 35 40 45 50

cag tac gcc ccg agg gtc ctg acg cag gct tcc aac ccc gtc gtc tgc 309
 Gln Tyr Ala Pro Arg Val Leu Thr Gln Ala Ser Asn Pro Val Val Cys
 55 60 65

acg cag ccc aaa tcc cca tcc ggg aca gtg tgc acc tca aag act aag 357
 Thr Gln Pro Lys Ser Pro Ser Gly Thr Val Cys Thr Ser Lys Thr Lys
 70 75 80

C1 aaa gca ctg tgc atc acc ttg acc ctg ggg acc ttc ctc gtg gga gct 405
 Lys Ala Leu Cys Ile Thr Leu Thr Leu Gly Thr Phe Leu Val Gly Ala
 85 90 95

gcg ctg gcc gct ggc cta ctc tgg aag ttc atg ggc agc aag tgc tcc 453
 Ala Leu Ala Ala Gly Leu Leu Trp Lys Phe Met Gly Ser Lys Cys Ser
 100 105 110

aac tct ggg ata gag tgc gac tcc tca ggt acc tgc atc aac ccc tct 501
 Asn Ser Gly Ile Glu Cys Asp Ser Ser Gly Thr Cys Ile Asn Pro Ser
 115 120 125 130

aac tgg tgt gat ggc gtg tca cac tgc ccc ggc ggg gag gac gag aat 549
 Asn Trp Cys Asp Gly Val Ser His Cys Pro Gly Gly Glu Asp Glu Asn
 135 140 145

cgg tgt gtt cgc ctc tac gga cca aac ttc atc ctt cag gtg tac tca 597
 Arg Cys Val Arg Leu Tyr Gly Pro Asn Phe Ile Leu Gln Val Tyr Ser
 150 155 160

tct cag agg aag tcc tgg cac cct gtg tgc caa gac gac tgg aac gag 645
 Ser Gln Arg Lys Ser Trp His Pro Val Cys Gln Asp Asp Trp Asn Glu
 165 170 175

aac tac ggg cgg gcg gcc tgc agg gac atg ggc tat aag aat aat ttt 693
 Asn Tyr Gly Arg Ala Ala Cys Arg Asp Met Gly Tyr Lys Asn Asn Phe
 180 185 190

tac tct agc caa gga ata gtg gat gac agc gga tcc acc agc ttt atg 741
 Tyr Ser Ser Gln Gly Ile Val Asp Asp Ser Gly Ser Thr Ser Phe Met
 195 200 205 210

aaa ctg aac aca agt gcc ggc aat gtc gat atc tat aaa aaa ctg tac 789
 Lys Leu Asn Thr Ser Ala Gly Asn Val Asp Ile Tyr Lys Lys Leu Tyr
 215 220 225

cac agt gat gcc tgt tct tca aaa gca gtg gtt tct tta cgc tgt ata 837
 His Ser Asp Ala Cys Ser Ser Lys Ala Val Val Ser Leu Arg Cys Ile
 230 235 240

gcc tgc ggg gtc aac ttg aac tca agc cgc cag agc agg att gtg ggc 885

Ala Cys Gly Val Asn Leu Asn Ser Ser Arg Gln Ser Arg Ile Val Gly
245 250 255

ggc gag agc gcg ctc ccg ggg gcc tgg ccc tgg cag gtc agc ctg cac 933
Gly Glu Ser Ala Leu Pro Gly Ala Trp Pro Trp Gln Val Ser Leu His
260 265 270

gtc cag aac gtc cac gtg tgc gga ggc tcc atc atc acc ccc gag tgg 981
Val Gln Asn Val His Val Cys Gly Gly Ser Ile Ile Thr Pro Glu Trp
275 280 285 290

atc gtg aca gcc gcc cac tgc gtg gaa aaa cct ctt aac aat cca tgg 1029
Ile Val Thr Ala Ala His Cys Val Glu Lys Pro Leu Asn Asn Pro Trp
295 300 305

cat tgg acg gca ttt gcg ggg att ttg aga caa tct ttc atg ttc tat 1077
His Trp Thr Ala Phe Ala Gly Ile Leu Arg Gln Ser Phe Met Phe Tyr
310 315 320

gga gcc gga tac caa gta gaa aaa gtg att tct cat cca aat tat gac 1125
Gly Ala Gly Tyr Gln Val Glu Lys Val Ile Ser His Pro Asn Tyr Asp
325 330 335

tcc aag acc aag aac aat gac att gcg ctg atg aag ctg cag aag cct 1173
Ser Lys Thr Lys Asn Asn Asp Ile Ala Leu Met Lys Leu Gln Lys Pro
340 345 350

ctg act ttc aac gac cta gtg aaa cca gtg tgt ctg ccc aac cca ggc 1221
Leu Thr Phe Asn Asp Leu Val Lys Pro Val Cys Leu Pro Asn Pro Gly
355 360 365 370

atg atg ctg cag cca gaa cag ctc tgc tgg att tcc ggg tgg ggg gcc 1269
Met Met Leu Gln Pro Glu Gln Leu Cys Trp Ile Ser Gly Trp Gly Ala
375 380 385

acc gag gag aaa ggg aag acc tca gaa gtg ctg aac gct gcc aag gtg 1317
Thr Glu Glu Lys Gly Lys Thr Ser Glu Val Leu Asn Ala Ala Lys Val
390 395 400

ctt ctc att gag aca cag aga tgc aac agc aga tat gtc tat gac aac 1365
Leu Leu Ile Glu Thr Gln Arg Cys Asn Ser Arg Tyr Val Tyr Asp Asn
405 410 415

ctg atc aca cca gcc atg atc tgt gcc ggc ttc ctg cag ggg aac gtc 1413
Leu Ile Thr Pro Ala Met Ile Cys Ala Gly Phe Leu Gln Gly Asn Val
420 425 430

gat tct tgc cag ggt gac agt gga ggg cct ctg gtc act tcg aag aac 1461
Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Thr Ser Lys Asn
435 440 445 450

aat atc tgg tgg ctg ata ggg gat aca agc tgg ggt tct ggc tgt gcc 1509
Asn Ile Trp Trp Leu Ile Gly Asp Thr Ser Trp Gly Ser Gly Cys Ala
455 460 465

aaa gct tac aga cca gga gtg tac ggg aat gtg atg gta ttc acg gac 1557
Lys Ala Tyr Arg Pro Gly Val Tyr Gly Asn Val Met Val Phe Thr Asp

470

475

480

tgg att tat cga caa atg agg gca gac ggc t aatccacatg gtcttcgtcc 1608
 Trp Ile Tyr Arg Gln Met Arg Ala Asp Gly
 485 490

ttgacgtcgt tttaacaagaa aacaatgggg ctgggttttgc ttccccgtgc atgatttact 1668
 cttagagatg attcagaggt cacttcattt ttattaaaca gtgaacttgt ctggcaaaaa 1728
 aaaaaaaaaa 1738

<210> 2

<211> 492

<212> PRT

<213> Homo sapiens

<400> 2

Met Ala Leu Asn Ser Gly Ser Pro Pro Ala Ile Gly Pro Tyr Tyr Glu
 1 5 10 15
 Asn His Gly Tyr Gln Pro Glu Asn Pro Tyr Pro Ala Gln Pro Thr Val
 20 25 30
 Val Pro Thr Val Tyr Glu Val His Pro Ala Gln Tyr Tyr Pro Ser Pro
 35 40 45
 Val Pro Gln Tyr Ala Pro Arg Val Leu Thr Gln Ala Ser Asn Pro Val
 50 55 60
 Val Cys Thr Gln Pro Lys Ser Pro Ser Gly Thr Val Cys Thr Ser Lys
 65 70 75 80
 Thr Lys Lys Ala Leu Cys Ile Thr Leu Thr Leu Gly Thr Phe Leu Val
 85 90 95
 Gly Ala Ala Leu Ala Ala Gly Leu Leu Trp Lys Phe Met Gly Ser Lys
 100 105 110
 Cys Ser Asn Ser Gly Ile Glu Cys Asp Ser Ser Gly Thr Cys Ile Asn
 115 120 125
 Pro Ser Asn Trp Cys Asp Gly Val Ser His Cys Pro Gly Gly Glu Asp
 130 135 140
 Glu Asn Arg Cys Val Arg Leu Tyr Gly Pro Asn Phe Ile Leu Gln Val
 145 150 155 160
 Tyr Ser Ser Gln Arg Lys Ser Trp His Pro Val Cys Gln Asp Asp Trp
 165 170 175
 Asn Glu Asn Tyr Gly Arg Ala Ala Cys Arg Asp Met Gly Tyr Lys Asn
 180 185 190
 Asn Phe Tyr Ser Ser Gln Gly Ile Val Asp Asp Ser Gly Ser Thr Ser
 195 200 205
 Phe Met Lys Leu Asn Thr Ser Ala Gly Asn Val Asp Ile Tyr Lys Lys
 210 215 220
 Leu Tyr His Ser Asp Ala Cys Ser Ser Lys Ala Val Val Ser Leu Arg
 225 230 235 240
 Cys Ile Ala Cys Gly Val Asn Leu Asn Ser Ser Arg Gln Ser Arg Ile
 245 250 255
 Val Gly Gly Glu Ser Ala Leu Pro Gly Ala Trp Pro Trp Gln Val Ser
 260 265 270
 Leu His Val Gln Asn Val His Val Cys Gly Gly Ser Ile Ile Thr Pro
 275 280 285
 Glu Trp Ile Val Thr Ala Ala His Cys Val Glu Lys Pro Leu Asn Asn
 290 295 300
 Pro Trp His Trp Thr Ala Phe Ala Gly Ile Leu Arg Gln Ser Phe Met
 305 310 315 320
 Phe Tyr Gly Ala Gly Tyr Gln Val Glu Lys Val Ile Ser His Pro Asn

Tyr Asp Ser Lys Thr Lys Asn Asn Asp Ile Ala Leu Met Lys Leu Gln
 325 330 335
 340 345 350
 Lys Pro Leu Thr Phe Asn Asp Leu Val Lys Pro Val Cys Leu Pro Asn
 355 360 365
 Pro Gly Met Met Leu Gln Pro Glu Gln Leu Cys Trp Ile Ser Gly Trp
 370 375 380
 Gly Ala Thr Glu Glu Lys Gly Lys Thr Ser Glu Val Leu Asn Ala Ala
 385 390 395 400
 Lys Val Leu Leu Ile Glu Thr Gln Arg Cys Asn Ser Arg Tyr Val Tyr
 405 410 415
 Asp Asn Leu Ile Thr Pro Ala Met Ile Cys Ala Gly Phe Leu Gln Gly
 420 425 430
 Asn Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Thr Ser
 435 440 445
 Lys Asn Asn Ile Trp Trp Leu Ile Gly Asp Thr Ser Trp Gly Ser Gly
 450 455 460
 Cys Ala Lys Ala Tyr Arg Pro Gly Val Tyr Gly Asn Val Met Val Phe
 465 470 475 480
 Thr Asp Trp Ile Tyr Arg Gln Met Arg Ala Asp Gly
 485 490

<210> 3
 <211> 2479
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (57)...(1534)

<400> 3
 gtcattattga acattccaga tacctatcat tactcgatgc tgttgataac agcaag atg 59
 Met
 1

 gct ttg aac tca ggg tca cca cca gct att gga cct tac tat gaa aac 107
 Ala Leu Asn Ser Gly Ser Pro Pro Ala Ile Gly Pro Tyr Tyr Glu Asn
 5 10 15

 cat gga tac caa ccg gaa aac ccc tat ccc gca cag ccc act gtg gtc 155
 His Gly Tyr Gln Pro Glu Asn Pro Tyr Pro Ala Gln Pro Thr Val Val
 20 25 30

 ccc act gtc tac gag gtg cat ccg gct cag tac tac ccg tcc ccc gtg 203
 Pro Thr Val Tyr Glu Val His Pro Ala Gln Tyr Tyr Pro Ser Pro Val
 35 40 45

 ccc cag tac gcc ccg agg gtc ctg acg cag gct tcc aac ccc gtc gtc 251
 Pro Gln Tyr Ala Pro Arg Val Leu Thr Gln Ala Ser Asn Pro Val Val
 50 55 60 65

 tgc acg cag ccc aaa tcc cca tcc ggg aca gtg tgc acc tca aag act 299
 Cys Thr Gln Pro Lys Ser Pro Ser Gly Thr Val Cys Thr Ser Lys Thr
 70 75 80

 aag aaa gca ctg tgc atc acc ttg acc ctg ggg acc ttc ctc gtg gga 347

Lys Lys Ala Leu Cys Ile Thr Leu Thr Leu Gly Thr Phe Leu Val Gly
 85 90 95

gct gcg ctg gcc gct ggc cta ctc tgg aag ttc atg ggc agc aag tgc 395
 Ala Ala Leu Ala Ala Gly Leu Leu Trp Lys Phe Met Gly Ser Lys Cys
 100 105 110

tcc aac tct ggg ata gag tgc gac tcc tca ggt acc tgc atc aac ccc 443
 Ser Asn Ser Gly Ile Glu Cys Asp Ser Ser Gly Thr Cys Ile Asn Pro
 115 120 125

tct aac tgg tgt gat ggc gtg tca cac tgc ccc ggc ggg gag gac gag 491
 Ser Asn Trp Cys Asp Gly Val Ser His Cys Pro Gly Gly Glu Asp Glu
 130 135 140 145

aat cgg tgt gtt cgc ctc tac gga cca aac ttc atc ctt cag atg tac 539
 Asn Arg Cys Val Arg Leu Tyr Gly Pro Asn Phe Ile Leu Gln Met Tyr
 150 155 160

tca tct cag agg aag tcc tgg cac cct gtg tgc caa gac gac tgg aac 587
 Ser Ser Gln Arg Lys Ser Trp His Pro Val Cys Gln Asp Asp Trp Asn
 165 170 175

gag aac tac ggg cgg gcg gcc tgc agg gac atg ggc tat aag aat aat 635
 Glu Asn Tyr Gly Arg Ala Ala Cys Arg Asp Met Gly Tyr Lys Asn Asn
 180 185 190

ttt tac tct agc caa gga ata gtg gat gac agc gga tcc acc agc ttt 683
 Phe Tyr Ser Ser Gln Gly Ile Val Asp Asp Ser Gly Ser Thr Ser Phe
 195 200 205

atg aaa ctg aac aca agt gcc ggc aat gtc gat atc tat aaa aaa ctg 731
 Met Lys Leu Asn Thr Ser Ala Gly Asn Val Asp Ile Tyr Lys Lys Leu
 210 215 220 225

tac cac agt gat gcc tgt tct tca aaa gca gtg gtt tct tta cgc tgt 779
 Tyr His Ser Asp Ala Cys Ser Ser Lys Ala Val Val Ser Leu Arg Cys
 230 235 240

tta gcc tgc ggg gtc aac ttg aac tca agc cgc cag agc agg atc gtg 827
 Leu Ala Cys Gly Val Asn Leu Asn Ser Ser Arg Gln Ser Arg Ile Val
 245 250 255

ggc ggt gag agc gcg ctc ccg ggg gcc tgg ccc tgg cag gtc agc ctg 875
 Gly Gly Glu Ser Ala Leu Pro Gly Ala Trp Pro Trp Gln Val Ser Leu
 260 265 270

cac gtc cag aac gtc cac gtg tgc gga ggc tcc atc atc acc ccc gag 923
 His Val Gln Asn Val His Val Cys Gly Gly Ser Ile Ile Thr Pro Glu
 275 280 285

tgg atc gtg aca gcc gcc cac tgc gtg gaa aaa cct ctt aac aat cca 971
 Trp Ile Val Thr Ala Ala His Cys Val Glu Lys Pro Leu Asn Asn Pro
 290 295 300 305

tgg cat tgg acg gca ttt gcg ggg att ttg aga caa tct ttc atg ttc 1019
 Trp His Trp Thr Ala Phe Ala Gly Ile Leu Arg Gln Ser Phe Met Phe

	310	315	320	
	tat gga gcc gga tac caa gta caa aaa gtg att tct cat cca aat tat			1067
	Tyr Gly Ala Gly Tyr Gln Val Gln Lys Val Ile Ser His Pro Asn Tyr			
	325	330	335	
	gac tcc aag acc aag aac aat gac att gcg ctg atg aag ctg cag aag			1115
	Asp Ser Lys Thr Lys Asn Asn Asp Ile Ala Leu Met Lys Leu Gln Lys			
	340	345	350	
	cct ctg act ttc aac gac cta gtg aaa cca gtg tgt ctg ccc aac cca			1163
	Pro Leu Thr Phe Asn Asp Leu Val Lys Pro Val Cys Leu Pro Asn Pro			
	355	360	365	
C	ggc atg atg ctg cag cca gaa cag ctc tgc tgg att tcc ggg tgg ggg			1211
	Gly Met Met Leu Gln Pro Glu Gln Leu Cys Trp Ile Ser Gly Trp Gly			
	370	375	380	385
	gcc acc gag gag aaa ggg aag acc tca gaa gtg ctg aac gct gcc aag			1259
	Ala Thr Glu Glu Lys Gly Lys Thr Ser Glu Val Leu Asn Ala Ala Lys			
	390	395	400	
	gtg ctt ctc att gag aca cag aga tgc aac agc aga tat gtc tat gac			1307
	Val Leu Leu Ile Glu Thr Gln Arg Cys Asn Ser Arg Tyr Val Tyr Asp			
	405	410	415	
	aac ctg atc aca cca gcc atg atc tgt gcc ggc ttc ctg cag ggg aac			1355
	Asn Leu Ile Thr Pro Ala Met Ile Cys Ala Gly Phe Leu Gln Gly Asn			
	420	425	430	
	gtc gat tct tgc cag ggt gac agt gga ggg cct ctg gtc act tcg aac			1403
	Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Thr Ser Asn			
	435	440	445	
	aac aat atc tgg tgg ctg ata ggg gat aca agc tgg ggt tct ggc tgt			1451
	Asn Asn Ile Trp Trp Leu Ile Gly Asp Thr Ser Trp Gly Ser Gly Cys			
	450	455	460	465
	gcc aaa gct tac aga cca gga gtg tac ggg aat gtg atg gta ttc acg			1499
	Ala Lys Ala Tyr Arg Pro Gly Val Tyr Gly Asn Val Met Val Phe Thr			
	470	475	480	
	gac tgg att tat cga caa atg aag gca aac ggc ta atccacatgg			1544
	Asp Trp Ile Tyr Arg Gln Met Lys Ala Asn Gly			
	485	490		
	tcttcgtcct tgacgtcggt ttacaagaaa acaatggggc tggttttgct tccccgtgca			1604
	tgatttactc ttagagatga ttcagaggtc acttcatttt tattaaacag tgaacttgct			1664
	tggctttggc actctctgcc atactgtgca ggctgcagt gctcccctgc ccagcctgct			1724
	ctccctaacc ccttgccgc aaggggtgat ggccggctgg ttgtgggcac tggcgggtcaa			1784
	ttgtggaagg aagaggggtg gaggtgccc ccattgagat ctctctgctg agtcctttcc			1844
	aggggccaat tttggatgag catggagctg tcacttctca gctgctggat gacttgagat			1904
	gaaaaaggag agacatggaa agggagacag ccaggtggca cctgcagcgg ctgccctctg			1964
	gggccacttg gtagtgctcc cagcctactt cacaagggga ttttgctgat gggttcttag			2024
	agccttagca gccctggatg gtggccagaa ataaaggac cagcccttca tgggtggtga			2084
	cgtggtagtc acttgtaagg ggaacagaaa catttttgtt cttatggggg gagaatatag			2144
	acagtgccct tgggtgcgagg gaagcaattg aaaagggaact tgccctgagc actcctggtg			2204

caggctctcca cctgcacatt ggggtggggct cctgggaggg agactcagcc ttctctctca 2264
 tcctccctga ccctgctcct agcaccctgg agagtgaatg ccccttggtc cctggcaggg 2324
 cgccaagttt ggcacatgt cggcctcttc aggectgata gtcattggaa attgaggtcc 2384
 atgggggaaa tcaaggatgc tcagtttaag gtacactgtt tccatgttat gtttctacac 2444
 attgatgggtg gtgacctga gttcaaagcc atctt 2479

<210> 4
 <211> 492
 <212> PRT
 <213> Homo sapiens

<400> 4

Met Ala Leu Asn Ser Gly Ser Pro Pro Ala Ile Gly Pro Tyr Tyr Glu
 1 5 10 15
 Asn His Gly Tyr Gln Pro Glu Asn Pro Tyr Pro Ala Gln Pro Thr Val
 20 25 30
 Val Pro Thr Val Tyr Glu Val His Pro Ala Gln Tyr Tyr Pro Ser Pro
 35 40 45
 Val Pro Gln Tyr Ala Pro Arg Val Leu Thr Gln Ala Ser Asn Pro Val
 50 55 60
 Val Cys Thr Gln Pro Lys Ser Pro Ser Gly Thr Val Cys Thr Ser Lys
 65 70 75 80
 Thr Lys Lys Ala Leu Cys Ile Thr Leu Thr Leu Gly Thr Phe Leu Val
 85 90 95
 Gly Ala Ala Leu Ala Ala Gly Leu Leu Trp Lys Phe Met Gly Ser Lys
 100 105 110
 Cys Ser Asn Ser Gly Ile Glu Cys Asp Ser Ser Gly Thr Cys Ile Asn
 115 120 125
 Pro Ser Asn Trp Cys Asp Gly Val Ser His Cys Pro Gly Gly Glu Asp
 130 135 140
 Glu Asn Arg Cys Val Arg Leu Tyr Gly Pro Asn Phe Ile Leu Gln Met
 145 150 155 160
 Tyr Ser Ser Gln Arg Lys Ser Trp His Pro Val Cys Gln Asp Asp Trp
 165 170 175
 Asn Glu Asn Tyr Gly Arg Ala Ala Cys Arg Asp Met Gly Tyr Lys Asn
 180 185 190
 Asn Phe Tyr Ser Ser Gln Gly Ile Val Asp Asp Ser Gly Ser Thr Ser
 195 200 205
 Phe Met Lys Leu Asn Thr Ser Ala Gly Asn Val Asp Ile Tyr Lys Lys
 210 215 220
 Leu Tyr His Ser Asp Ala Cys Ser Ser Lys Ala Val Val Ser Leu Arg
 225 230 235 240
 Cys Leu Ala Cys Gly Val Asn Leu Asn Ser Ser Arg Gln Ser Arg Ile
 245 250 255
 Val Gly Gly Glu Ser Ala Leu Pro Gly Ala Trp Pro Trp Gln Val Ser
 260 265 270
 Leu His Val Gln Asn Val His Val Cys Gly Gly Ser Ile Ile Thr Pro
 275 280 285
 Glu Trp Ile Val Thr Ala Ala His Cys Val Glu Lys Pro Leu Asn Asn
 290 295 300
 Pro Trp His Trp Thr Ala Phe Ala Gly Ile Leu Arg Gln Ser Phe Met
 305 310 315 320
 Phe Tyr Gly Ala Gly Tyr Gln Val Gln Lys Val Ile Ser His Pro Asn
 325 330 335
 Tyr Asp Ser Lys Thr Lys Asn Asn Asp Ile Ala Leu Met Lys Leu Gln
 340 345 350
 Lys Pro Leu Thr Phe Asn Asp Leu Val Lys Pro Val Cys Leu Pro Asn

355 360 365
 Pro Gly Met Met Leu Gln Pro Glu Gln Leu Cys Trp Ile Ser Gly Trp
 370 375 380
 Gly Ala Thr Glu Glu Lys Gly Lys Thr Ser Glu Val Leu Asn Ala Ala
 385 390 395 400
 Lys Val Leu Leu Ile Glu Thr Gln Arg Cys Asn Ser Arg Tyr Val Tyr
 405 410 415
 Asp Asn Leu Ile Thr Pro Ala Met Ile Cys Ala Gly Phe Leu Gln Gly
 420 425 430
 Asn Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Thr Ser
 435 440 445
 Asn Asn Asn Ile Trp Trp Leu Ile Gly Asp Thr Ser Trp Gly Ser Gly
 450 455 460
 Cys Ala Lys Ala Tyr Arg Pro Gly Val Tyr Gly Asn Val Met Val Phe
 465 470 475 480
 Thr Asp Trp Ile Tyr Arg Gln Met Lys Ala Asn Gly
 485 490

<210> 5
 <211> 388
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> misc_feature
 <222> (1)...(388)
 <223> n = A,T,C or G

<400> 5
 gatcttcctg ctgagtcctt tccaggggcc aattttggat gagcatggag ctgtcacctc 60
 tcagctgctg gatgacttga gatgaaaaag gagagacatg gaaagggaga cagccaggtg 120
 gcacctgcag cggtgcccct ctggggccac ttggtagtgt ccccgacctt cctctccaca 180
 aggggatttt gctgatgggt tcttanagcc ttagcagccc tggatgggtg ccagaaataa 240
 agggaccagc cttcatggg tggtagctg gtantcactt gtaaggggaa cagaaacatt 300
 tttgttctta tggggtgaga atatagacag tgcccttggt gcgaggggaa caattgaaaa 360
 ggaacttgcc ctgagcactc ctggtgca 388

<210> 6
 <211> 14
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> cDNA Synthesis Primer

<400> 6
 ttttgtacaa gctt 14

<210> 7
 <211> 44
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA Adaptor 1

<400> 7

ctaatacgac tcactatagg gctcgagcgg ccgcccgggc aggt 44

<210> 8
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA Adaptor 2

<400> 8
gtaatacgac tcactatagg gcagcgtggt cgcggccgag gt 42

<210> 9
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primer 1

<400> 9
ctaatacgac tcactatagg gc 22

<210> 10
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Nester PCR Primer (NP) 1

<400> 10
tcgagcggcc gcccgggcag gt 22

<210> 11
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Nester PCR Primer (NP) 2

<400> 11
agcgtggtcg cggccgaggt 20

<210> 12
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> RT-PCR Primer 1A

<400> 12
agtcttcctg ctgagtcctt tcc 23

<210> 13
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> RT-PCR Primer 1B

<400> 13
caagggcact gtctatatattc tcacc

25

<210> 14
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA Adaptor 1B

<400> 14
ggcccgtcca

10

<210> 15
<211> 8
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA Adaptor 2B

<400> 15
cggctcca

8

<210> 16
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> GST Primer 1

<400> 16
ttgaattcca aaccagtgtg tctgccc

27

<210> 17
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> GST Primer 2

<400> 17
aagctcgagt cgtcaccctg gcaagaat

28

<210> 18
<211> 18

<212> DNA
<213> Artificial Sequence

<220>
<223> Mutagenic Primer 1

<400> 18
ggccctccag cgtcaccc

18

<210> 19
<211> 27
<212> DNA
<213> Artificial Sequence

C1
<220>
<223> Mutagenic Primer 2

<400> 19
ccgcaggcta tacattgtaa agaaacc

27

<210> 20
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Mutagenic Primer 3

<400> 20
tcctgctctg ttggcttgag ttca

24

<210> 21
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Mutagenic Primer 4

<400> 21
cccacaatct ggctctggcg

20

<210> 22
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Mutagenic Primer 5

<400> 22
cgaattcgca agatggcttt gaac

24

<210> 23
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
 <223> Mutagenic Primer 6

 <400> 23
 ggggtgacgct ggagggcc 18

 <210> 24
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Mutagenic Primer 7

 <400> 24
 ggtttcttta caatgtatag cctgcgg 27

 <210> 25
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Mutagenic Primer 8

 <400> 25
 tgaactcaag ccaacagagc agga 24

 <210> 26
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Mutagenic Primer 9

 <400> 26
 cgccagagcc agattgtggg 20

 <210> 27
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Mutagenic Primer 10

 <400> 27
 cgtctagatt agccgtctgc cctca 25

 <210> 28
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>

<223> Actin Primer 1

<400> 28

atatcgccgc gctcgtcgtc gacaa

25

<210> 29

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Actin Primer 2

<400> 29

agccacacgc agtcattgt agaagg

26

<210> 30

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> N-myristoylation site

<400> 30

Gly Ser Pro Pro Ala Ile

1

5

<210> 31

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> N-myristoylation site

<400> 31

Gly Thr Val Cys Thr Ser

1

5

<210> 32

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> N-myristoylation site

<400> 32

Gly Ala Ala Leu Ala Ala

1

5

<210> 33

<211> 6

<212> PRT

<213> Artificial Sequence

<220>
<223> N-myristoylation site

<400> 33
Gly Ser Lys Cys Ser Asn
1 5

<210> 34
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> N-myristoylation site

<400> 34
Gly Val Asn Leu Asn Ser
1 5

<210> 35
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> N-myristoylation site

<400> 35
Gly Gly Glu Ser Ala Leu
1 5

<210> 36
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> N-myristoylation site

<400> 36
Gly Asn Val Asp Ser Cys
1 5

<210> 37
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> N-myristoylation site

<400> 37
Gly Ser Gly Cys Ala Lys
1 5

<210> 38
<211> 6

<212> PRT
 <213> Artificial Sequence
 <220>
 <223> N-myristoylation site

<400> 38
 Gly Cys Ala Lys Ala Tyr
 1 5

<210> 39
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> N-myristoylation site

<400> 39
 Gly Val Tyr Gly Asn
 1 5

<210> 40
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> P-loop

<400> 40
 Ala Thr Glu Glu Lys Gly Lys Thr
 1 5

<210> 41
 <211> 23
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> LDL-receptor class A

<400> 41
 Cys Ile Asn Pro Ser Asn Trp Cys Asp Gly Val Ser His Cys Pro Gly
 1 5 10 15
 Gly Glu Asp Glu Asn Arg Cys
 20

<210> 42
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Serine proteases, trypsin family, histidine active
 site

<400> 42

Val Thr Ala Ala His Cys

1

5

<210> 43

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Serine proteases, trypsin family, histidine active
site

<400> 43

Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val

1

5

10